EXHIBIT

2

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO1 488 aa Sequence 2: SEQIDNO3. 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 96

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10380

Alignment Score 2880

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200

CLUSTAL	W	(1.82)	multiple	sequence	alignment
			•		

SEQIDNO1	KEIAVII DDIAVII DO VOLO I I I I I I I I I I I I I I I I I I	60
SEQIDNO3.	KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV	60

SEOIDNO1	GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTKG	120
SEQIDNO3.	GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG	120
SEQIENCS.	*********	
SEOIDNO1	SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS	180
SEQIDNO1	SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS	180
SEQIDNOS.	***************	
CHOTOMO1	. AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSYVKGLADGAGDLVTAFTL	240
SEQIDNO1	AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL	
SEQIDNO3.	**************************************	240

	HQYYFDGNTSDVSTYLDATYFKKLQQLFDKVKDVLKNSQHKDKPLWLGETSSGYNSGTKD	300
SEQIDNO1	HQYYFDGNTSDVSIYLDATYFKKLOOLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED	300
SEQIDNO3.	*********** **************************	300 ,

CROTONO1	VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV	360
SEQIDNO1		360
SEQIDNO3.	\SDRY\SGFLIDDKLGLSAANN\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	300

GEOTENIO1	GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIDQYGG	420
SEQIDNO1	GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG	420
SEQIDNO3.	**************************************	420

CECTDNO1	KKIYSYILTPEGGOLTSOKVLLNGKELKLVSDQLPELNANESKTSFTLSPKTFGFFVVSD	480
SEQIDNO1	KKIYSYILTPEGGOLTSOKVLLNGKELNLVSDOLPELNADESKTSFTLSPKTFGFFVVSD	480
SEQIDNO3.	**************************************	400
•	**************************************	•
CEOTONO3	ANTITACIVE 400	
SEQIDNO1	ANVEACKK 488	
SEQIDNO3.	ANVEACKK 488	



CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO3 488 aa Sequence 2: SEQIDNO5 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 97

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10465

Alignment Score 2927

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200

	The state of the s		
SEOIDNO3	KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWAPFDITSPKLFKLLEGLSPGYFRV	60	
SEQIDNO5	KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV	60	

	•		
SEQIDNO3	${\tt GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG}$	120	
SEQIDNO5	${\tt GGTFANRLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG}$	120	
	***** *************		
SEQIDNO3	SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS	180	
SEQIDNO5	SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNGPDHTS	180	

CTOIDNO?	AHNLTEKOVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL	240	
SEQIDNO3	AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL		
SEQIDNO5	**************************************	240	
SEQIDNO3	HOYYFDGNTSDVSIYLDATYFKKLOOLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED	300	
SEOIDNO5		300	

	•		
SEQIDNO3	VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV		
SEQIDNO5	VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYSGYYGPLDKNTLEPNPDYWLMHVHNSLV	360	

•	·		
SEQIDNO3	GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG	420	
SEQIDNO5	GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIGQYSG	420	

SEOIDNO3.	KKIYSYILTPEGGOLTSOKVLLNGKELNLVSDOLPELNADESKTSFTLSPKTFGFFVVSD	480	
SEQIDNOS SEOIDNOS	KKIYSYILTPEGGOLTSOKVLLNGKELNLVSDOLPOLNADESKTSFTLSPKTFGFFVVSD	480	
020121103	***********		
SEQIDNO3	ANVEACKK 488		
SEQIDNO5	ANVEACKK 488		

CLUSTAL W (1.82) multiple sequence alignment

CLUSTAL W (1.82) Multiple Sequence Alignments



Sequence format is Pearson

Sequence 1: SEQIDNO3 488 aa Sequence 2: SEQIDNO7 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 94

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10323

Alignment Score 2848

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200

CLUSTAL W (1.82) multiple sequence alignment	
SEQIDNO3 SEQIDNO7	KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV	
SEQIDNO3 SEQIDNO7	GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG	
SEQIDNO3 SEQIDNO7	SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS ************************************	180 180
SEQIDNO3 SEQIDNO7	AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL ************************************	
SEQIDNO3 SEQIDNO7	HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD	
SEQIDNO3 SEQIDNO7	VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV ************************************	
SEQIDNO3 SEQIDNO7	GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG ******** :***************************	
SEQIDNO3 SEQIDNO7	KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD ***********************************	
SEQIDNO3 SEQIDNO7	ANVEACKK 488 ANVEACKK 488	